

SEQUENCE LISTING

<110> Powers, Scott
Yang, Jianxin
Cutler, Gene
Tularik Inc.

<120> Novel G-Protein Coupled Receptors

<130> 018781-004730US

<140> US Not yet assigned

<141> Not yet assigned

<150> US 09/524,730

<151> 2000-03-14

<150> US 09/546,986

<151> 2001-04-11

<160> 23

<170> PatentIn Ver. 2.1

<210> 1

<211> 1035

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (42) .. (974)

<223> human breast cancer amplified G-protein coupled
receptor 1 (BCA-GPCR-1)

<400> 1

agtgccagaa aatgccgcaa catgaaaagt gacaaccata g ctc tta ggg gac tcc 56
Leu Leu Gly Asp Ser
1 5

cct aaa gcc ttc atc ctt ctg ggt gtg tct gac agg ccg tgg ctg gaa 104
Pro Lys Ala Phe Ile Leu Leu Gly Val Ser Asp Arg Pro Trp Leu Glu
10 15 20

ctc cct ctc ttt gtg gtc ctc ctg ctg tcc tat gtg ctg gcc atg ttg 152
Leu Pro Leu Phe Val Val Leu Leu Ser Tyr Val Leu Ala Met Leu
25 30 35

ggg aac gtc gcc atc atc ctg gca tcc cgg gtg gat cct caa ctc cac 200
Gly Asn Val Ala Ile Ile Leu Ala Ser Arg Val Asp Pro Gln Leu His
40 45 50

agc ccc atg tac atc ttc ctc agt cac ctg tcc ttc ctg gac ctc tgc 248
Ser Pro Met Tyr Ile Phe Leu Ser His Leu Ser Phe Leu Asp Leu Cys
55 60 65

tac acc acc acg aca gtc cct cag atg ctg gtc aac atg ggc agt tcc 296
Tyr Thr Thr Thr Thr Val Pro Gln Met Leu Val Asn Met Gly Ser Ser
70 75 80 85

<210> 2
 <211> 310
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human breast cancer amplified G-protein coupled
 receptor 1 (BCA-GPCR-1)

<400> 2

```

Leu Leu Gly Asp Ser Pro Lys Ala Phe Ile Leu Leu Gly Val Ser Asp
 1           5           10           15
Arg Pro Trp Leu Glu Leu Pro Leu Phe Val Val Leu Leu Leu Ser Tyr
      20           25           30
Val Leu Ala Met Leu Gly Asn Val Ala Ile Ile Leu Ala Ser Arg Val
      35           40           45
Asp Pro Gln Leu His Ser Pro Met Tyr Ile Phe Leu Ser His Leu Ser
      50           55           60
Phe Leu Asp Leu Cys Tyr Thr Thr Thr Val Pro Gln Met Leu Val
      65           70           75           80
Asn Met Gly Ser Ser Gln Lys Thr Ile Ser Tyr Gly Gly Cys Thr Val
      85           90           95
Gln Tyr Ala Val Phe His Trp Leu Gly Cys Thr Glu Cys Ile Val Leu
      100          105          110
Ala Ala Met Ala Leu Asp Arg Tyr Val Ala Ser Cys Lys Pro Leu His
      115          120          125
Tyr Ala Val Leu Met His Arg Ala Leu Cys Gln Gln Leu Val Ala Leu
      130          135          140
Ala Trp Leu Ser Gly Phe Gly Asn Ser Phe Val Gln Val Val Leu Thr
      145          150          155          160
Val Gln Leu Pro Phe Cys Gly Arg Gln Val Leu Asn Asn Phe Phe Cys
      165          170          175          180
Glu Val Pro Ala Val Ile Lys Leu Ser Cys Ala Asp Thr Ala Met Asn
      180          185          190
Asp Thr Ile Leu Ala Val Leu Val Ala Phe Phe Val Leu Val Pro Leu
      195          200          205
Ala Leu Ile Leu Leu Ser Tyr Gly Phe Ile Ala Arg Ala Val Leu Arg
      210          215          220
Ile Gln Ser Ser Lys Gly Arg His Lys Ala Phe Gly Thr Cys Ser Ser
      225          230          235          240
His Leu Met Ile Val Ser Leu Phe Tyr Leu Pro Ala Ile Tyr Met Tyr
      245          250          255
Leu Gln Pro Pro Ser Ser Tyr Ser Gln Glu Gln Gly Lys Phe Ile Ser
      260          265          270
Leu Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Pro Phe Thr Tyr Thr
      275          280          285
Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg Arg Leu Leu Ala Arg
      290          295          300
Ile Trp Arg Leu Cys Gly
305          310

```

<210> 3
 <211> 1411
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (118)..(1113)
 <223> human breast cancer amplified G-protein coupled
 receptor 2 (BCA-GPCR-2)

<400> 3

```

ggcaaatggc tctcttaact tcacagacct gtaaattggaa attggagagt gccagatcat 60

ctgcatgtgc ccccttatct aattcttttg ttgtttctct gtaatagctg gtggatt    117

atg gga aag gac aat gcc agt tac cta cag gca ttc atc ctg gtg ggc    165
Met Gly Lys Asp Asn Ala Ser Tyr Leu Gln Ala Phe Ile Leu Val Gly
  1             5             10             15

tct tct gat cgg cct gga ctg gag aaa att ctc ttt gct gtt atc ttg    213
Ser Ser Asp Arg Pro Gly Leu Glu Lys Ile Leu Phe Ala Val Ile Leu
      20             25             30

atc ttc tgc atc ctg acc ctg gtg ggc aac act gcc atc atc ctc ttg    261
Ile Phe Cys Ile Leu Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Leu
      35             40             45

ctg gtc atg gat gtc agg ctc cac aca ccc atg tac ttc ttt ctt ggg    309
Leu Val Met Asp Val Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
      50             55             60

aat ctg tct ttc tta gat ctc tgc ttt aca gca agc att gcc cct cag    357
Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ala Ser Ile Ala Pro Gln
      65             70             75             80

ctg ctg tgg aac ctg ggg ggt cca gag aag acc atc acc tac cac ggc    405
Leu Leu Trp Asn Leu Gly Gly Pro Glu Lys Thr Ile Thr Tyr His Gly
      85             90             95

tgt gtg gcc caa ctc tac atc tac atg atg ctg ggc tcc acc gag tgc    453
Cys Val Ala Gln Leu Tyr Ile Tyr Met Met Leu Gly Ser Thr Glu Cys
      100             105             110

gtc ctc ctg gtt gtc atg tcc cat gac cgc tat gtg gcc gtc tgc cgg    501
Val Leu Leu Val Val Met Ser His Asp Arg Tyr Val Ala Val Cys Arg
      115             120             125

tcc ctg cac tac atg gca gtc atg cgc cca cat ctc tgc ctg cag ctg    549
Ser Leu His Tyr Met Ala Val Met Arg Pro His Leu Cys Leu Gln Leu
      130             135             140

gtg act gtg gcc tgg tgc tgt ggc ttc cta aac tcc ttc atc atg tgt    597
Val Thr Val Ala Trp Cys Cys Gly Phe Leu Asn Ser Phe Ile Met Cys
      145             150             155             160

cct cag acg atg cag ctc tcc cgg tgt gga cgt cgc agg gtg gac cac    645
Pro Gln Thr Met Gln Leu Ser Arg Cys Gly Arg Arg Arg Val Asp His
      165             170             175

ttc ctg tgt gag atg cct gct ctt att gcc atg tct tgt gag gaa acc    693
Phe Leu Cys Glu Met Pro Ala Leu Ile Ala Met Ser Cys Glu Glu Thr
      180             185             190

```

atg ctg gta gaa gcg att cac ctt tgc cct ggg ggt ggc tct cct cct 741
 Met Leu Val Glu Ala Ile His Leu Cys Pro Gly Gly Gly Ser Pro Pro
 195 200 205

ggt gcc gct ctc cct cat cct cat ctc tat ggc gtg att gca gcc gcg 789
 Gly Ala Ala Leu Pro His Pro His Leu Tyr Gly Val Ile Ala Ala Ala
 210 215 220

gtg ctg agg atg aag tca gca gca ggg cga aag aaa gcc ttc cac acc 837
 Val Leu Arg Met Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe His Thr
 225 230 235 240

tgc tct tct cac ctc aca gtg gtc tct ctc ttc tac gga acc atc atc 885
 Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
 245 250 255

tac gtg tac ctg aag ccg gcc aac agc tac tcc caa gat cag ggg aag 933
 Tyr Val Tyr Leu Lys Pro Ala Asn Ser Tyr Ser Gln Asp Gln Gly Lys
 260 265 270

ttc ctg act ctc ttc tac acc atc gtc att ccc agc atc aac ccc ctc 981
 Phe Leu Thr Leu Phe Tyr Thr Ile Val Ile Pro Ser Ile Asn Pro Leu
 275 280 285

atc tac act ttg agg aac aag gat gtg aag ggg acc atg aag aaa ctt 1029
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Thr Met Lys Lys Leu
 290 295 300

ctg ggg tgg gag aaa ggg gct ggg gag cct caa cga ggg gaa cac tct 1077
 Leu Gly Trp Glu Lys Gly Ala Gly Glu Pro Gln Arg Gly Glu His Ser
 305 310 315 320

agt aat gta gac agt ttg ctg gag tta ctc tct tag atgtgtctgt 1123
 Ser Asn Val Asp Ser Leu Leu Glu Leu Ser
 325 330

ggccatgtgg agaactaata ttcaaggagt agagtgaacg cgggtgggaa aatgctttcg 1183

agtttgaccc cgctcctctgc cctctggatg tgaagtgggtt tccttctgtt tgaagttgcc 1243

tgcttcagga tatctctgct gtatcttgca ctttccttgt ctttttgatt tatccacaac 1303

tgctggggac ttacaaaact aattcaatca cccaaaggca ctgggcagtc tgcagattat 1363

gtcatggatg tcaaataaaa attgagacaa catgaaaaaa aaaaaaaaaa 1411

<210> 4

<211> 331

<212> PRT

<213> Homo sapiens

<220>

<223> human breast cancer amplified G-protein coupled
receptor 2 (BCA-GPCR-2)

<400> 4

Met Gly Lys Asp Asn Ala Ser Tyr Leu Gln Ala Phe Ile Leu Val Gly
 1 5 10 15
 Ser Ser Asp Arg Pro Gly Leu Glu Lys Ile Leu Phe Ala Val Ile Leu
 20 25 30

Ile	Phe	Cys	Ile	Leu	Thr	Leu	Val	Gly	Asn	Thr	Ala	Ile	Ile	Leu	Leu
		35					40					45			
Leu	Val	Met	Asp	Val	Arg	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Gly
		50					55				60				
Asn	Leu	Ser	Phe	Leu	Asp	Leu	Cys	Phe	Thr	Ala	Ser	Ile	Ala	Pro	Gln
		65			70					75				80	
Leu	Leu	Trp	Asn	Leu	Gly	Gly	Pro	Glu	Lys	Thr	Ile	Thr	Tyr	His	Gly
			85						90					95	
Cys	Val	Ala	Gln	Leu	Tyr	Ile	Tyr	Met	Met	Leu	Gly	Ser	Thr	Glu	Cys
			100					105					110		
Val	Leu	Leu	Val	Val	Met	Ser	His	Asp	Arg	Tyr	Val	Ala	Val	Cys	Arg
		115					120					125			
Ser	Leu	His	Tyr	Met	Ala	Val	Met	Arg	Pro	His	Leu	Cys	Leu	Gln	Leu
		130					135				140				
Val	Thr	Val	Ala	Trp	Cys	Cys	Gly	Phe	Leu	Asn	Ser	Phe	Ile	Met	Cys
		145			150					155				160	
Pro	Gln	Thr	Met	Gln	Leu	Ser	Arg	Cys	Gly	Arg	Arg	Arg	Val	Asp	His
				165					170					175	
Phe	Leu	Cys	Glu	Met	Pro	Ala	Leu	Ile	Ala	Met	Ser	Cys	Glu	Glu	Thr
			180					185					190		
Met	Leu	Val	Glu	Ala	Ile	His	Leu	Cys	Pro	Gly	Gly	Gly	Ser	Pro	Pro
		195					200					205			
Gly	Ala	Ala	Leu	Pro	His	Pro	His	Leu	Tyr	Gly	Val	Ile	Ala	Ala	Ala
		210				215					220				
Val	Leu	Arg	Met	Lys	Ser	Ala	Ala	Gly	Arg	Lys	Lys	Ala	Phe	His	Thr
		225			230					235				240	
Cys	Ser	Ser	His	Leu	Thr	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Ile	Ile
				245					250					255	
Tyr	Val	Tyr	Leu	Lys	Pro	Ala	Asn	Ser	Tyr	Ser	Gln	Asp	Gln	Gly	Lys
			260					265					270		
Phe	Leu	Thr	Leu	Phe	Tyr	Thr	Ile	Val	Ile	Pro	Ser	Ile	Asn	Pro	Leu
		275					280					285			
Ile	Tyr	Thr	Leu	Arg	Asn	Lys	Asp	Val	Lys	Gly	Thr	Met	Lys	Lys	Leu
		290				295					300				
Leu	Gly	Trp	Glu	Lys	Gly	Ala	Gly	Glu	Pro	Gln	Arg	Gly	Glu	His	Ser
					310					315				320	
Ser	Asn	Val	Asp	Ser	Leu	Leu	Glu	Leu	Leu	Ser					
				325						330					

<210> 5
 <211> 1351
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (86)..(1108)
 <223> human breast cancer amplified G-protein coupled
 receptor 3-A (BCA-GPCR-3-A)

<400> 5
 gattgtgtct ctaaaaaaga ataacataaa atgaactaaa atacactttt aatgtttgct 60

 aactgatgta attgcttcat gtctc atg ccc tgt atg ccc tgt gct ctt ccc 112
 Met Pro Cys Met Pro Cys Ala Leu Pro
 1 5

 aca ggt ggc ctt ttg ccc cac ccc cag cat aca atg atg gaa ata gcc 160
 Thr Gly Gly Leu Leu Pro His Pro Gln His Thr Met Met Glu Ile Ala
 10 15 20 25

aat gtg agt tct cca gaa gtc ttt gtc ctc ctg ggc ttc tcc gca cga	208
Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu Gly Phe Ser Ala Arg	
30 35 40	
ccc tca cta gaa act gtc ctc ttc ata gtt gtc ttg agt ttt tac atg	256
Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val Leu Ser Phe Tyr Met	
45 50 55	
gta tcg atc ttg ggc aat ggc atc atc att ctg gtc tcc cat aca gat	304
Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu Val Ser His Thr Asp	
60 65 70	
gtg cac ctc cac aca cct atg tac ttc ttt ctt gcc aac ctc tcc ttc	352
Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser Phe	
75 80 85	
ctg gac atg agc ttc acc acg agc att gtc cca cag ctc ctg gct aac	400
Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro Gln Leu Leu Ala Asn	
90 95 100 105	
ctc tgg gga cca cag aaa acc ata agc tat gga ggg tgt gtg gtc cag	448
Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly Cys Val Val Gln	
110 115 120	
ttc tat atc tcc cat tgg ctg ggg gca acc gag tgt gtc ctg ctg gcc	496
Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys Val Leu Leu Ala	
125 130 135	
acc atg tcc tat gac cgc tac gct gcc atc tgc agg cca ctc cat tac	544
Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg Pro Leu His Tyr	
140 145 150	
act gtc att atg cat cca cag ctt tgc ctt ggg cta gct ttg gcc tcc	592
Thr Val Ile Met His Pro Gln Leu Cys Leu Gly Leu Ala Leu Ala Ser	
155 160 165	
tgg ctg ggg ggt ctg acc acc agc atg gtg ggc tcc acg ctc acc atg	640
Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly Ser Thr Leu Thr Met	
170 175 180 185	
ctc cta ccg ctg tgt ggg aac aat tgc atc gac cac ttc ttt tgc gag	688
Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His Phe Phe Cys Glu	
190 195 200	
atg ccc ctc att atg caa ctg gct tgt gtg gat acc agc ctc aat gag	736
Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr Ser Leu Asn Glu	
205 210 215	
atg gag atg tac ctg gcc agc ttt gtc ttt gtt gtc ctg cct ctg ggg	784
Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val Leu Pro Leu Gly	
220 225 230	
ctc atc ctg gtc tct tac ggc cac att gcc cgg gcc gtg ttg aag atc	832
Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala Val Leu Lys Ile	
235 240 245	
agg tca gca gaa ggg cgg aga aag gca ttc aac acc tgt tct tcc cac	880
Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Ser Ser His	
250 255 260 265	

```

gtg gct gtg gtg tct ctg ttt tac ggg agc atc atc ttc atg tat ctc 928
Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile Phe Met Tyr Leu
                270                275                280

cag cca gcc aag agc acc tcc cat gag cag ggc aag ttc ata gct ctg 976
Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys Phe Ile Ala Leu
                285                290                295

ttc tac acc gta gtc act cct gcg ttg aac cca ctt att tac acc ctg 1024
Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu
                300                305                310

agg aac acg gag gtg aag agc gcc ctc cgg cac atg gta tta gag aac 1072
Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His Met Val Leu Glu Asn
                315                320                325

tgc tgt ggc tct gca ggc aag ctg gcg caa att tag agactccagt 1118
Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile
330                335                340

gccttctgag aaggaagatc aagtttacat cgagcaaagt gaccttggaa gacagggcac 1178

ttgggatgtc gtttttcttc taatattggt tgagctcaag gtagatggaa atctgaaagg 1238

agtgtgctca tgccatttcc agaccaagaa aacacattta ttatttgcta attatcatag 1298

ttttgttcaa ttgcgttggt ggtttttgct atatatacac atgttgactg tca 1351

<210> 6
<211> 340
<212> PRT
<213> Homo sapiens

<220>
<223> human breast cancer amplified G-protein coupled
      receptor 3-A (BCA-GPCR-3-A)

<400> 6
Met Pro Cys Met Pro Cys Ala Leu Pro Thr Gly Gly Leu Leu Pro His
  1          5          10          15
Pro Gln His Thr Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val
  20          25          30
Phe Val Leu Leu Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu
  35          40          45
Phe Ile Val Val Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly
  50          55          60
Ile Ile Ile Leu Val Ser His Thr Asp Val His Leu His Thr Pro Met
  65          70          75          80
Tyr Phe Phe Leu Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr
  85          90          95
Ser Ile Val Pro Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr
  100         105         110
Ile Ser Tyr Gly Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu
  115         120         125
Gly Ala Thr Glu Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr
  130         135         140
Ala Ala Ile Cys Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln
  145         150         155         160
Leu Cys Leu Gly Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr
  165         170         175

```


Ser Met Val Gly Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn
 180 185 190
 Asn Cys Ile Asp His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu
 195 200 205
 Ala Cys Val Asp Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser
 210 215 220
 Phe Val Phe Val Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly
 225 230 235 240
 His Ile Ala Arg Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg
 245 250 255
 Lys Ala Phe Asn Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe
 260 265 270
 Tyr Gly Ser Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser
 275 280 285
 His Glu Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro
 290 295 300
 Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser
 305 310 315 320
 Ala Leu Arg His Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys
 325 330 335
 Leu Ala Gln Ile
 340

<210> 7

<211> 1065

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(1030)

<223> human breast cancer amplified G-protein coupled
receptor 4 (BCA-GPCR-4)

<400> 7

attgtcactc atttaaccct atgtg atg tgt tat ctt tct cag cta tgc ctc 52
 Met Cys Tyr Leu Ser Gln Leu Cys Leu
 1 5

agc ctt ggg gaa cac act tta cat atg ggg atg gtg aga cat acc aat 100
 Ser Leu Gly Glu His Thr Leu His Met Gly Met Val Arg His Thr Asn
 10 15 20 25

gag agc aac cta gca ggt ttc atc ctt tta ggg ttt tct gat tat gct 148
 Glu Ser Asn Leu Ala Gly Phe Ile Leu Leu Gly Phe Ser Asp Tyr Ala
 30 35 40

cag tta cag aag gtt cta ttt gtg ctc ata ttg att ctg tat tta cta 196
 Gln Leu Gln Lys Val Leu Phe Val Leu Ile Leu Ile Leu Tyr Leu Leu
 45 50 55

act att ttg ggg aat acc acc atc att ctg gtt tct cgt ctg gaa ccc 244
 Thr Ile Leu Gly Asn Thr Thr Ile Ile Leu Val Ser Arg Leu Glu Pro
 60 65 70

aag ctt cat atg ccg atg tat ttc ttc ctt tct cat ctc tcc ttc ctg 292
 Lys Leu His Met Pro Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu
 75 80 85

tac cgc tgc ttc acc agc agt gtt att ccc cag ctc ctg gta aac ctg	340
Tyr Arg Cys Phe Thr Ser Ser Val Ile Pro Gln Leu Leu Val Asn Leu	
90 95 100 105	
tgg gaa ccc atg aaa act atc gcc tat ggt ggc tgt ttg gtt cac ctt	388
Trp Glu Pro Met Lys Thr Ile Ala Tyr Gly Gly Cys Leu Val His Leu	
110 115 120	
tac aac tcc cat gcc ctg gga tcc act gag tgc gtc ctc ccg gct ctg	436
Tyr Asn Ser His Ala Leu Gly Ser Thr Glu Cys Val Leu Pro Ala Leu	
125 130 135	
atg tcc tgt gac cgc tat gtg gct gtc tgc cgt cct ctc cat tac act	484
Met Ser Cys Asp Arg Tyr Val Ala Val Cys Arg Pro Leu His Tyr Thr	
140 145 150	
gtc tta atg cat atc cat ctc tgc atg gcc ttg gca tct atg gca tgg	532
Val Leu Met His Ile His Leu Cys Met Ala Leu Ala Ser Met Ala Trp	
155 160 165	
ctc agt gga ata gcc acc acc ctg gta cag tcc acc ctc acc ctg cag	580
Leu Ser Gly Ile Ala Thr Thr Leu Val Gln Ser Thr Leu Thr Leu Gln	
170 175 180 185	
ctg ccc ttc tgt ggg cat cgc caa gtg gat cat ttc atc tgc gag gtc	628
Leu Pro Phe Cys Gly His Arg Gln Val Asp His Phe Ile Cys Glu Val	
190 195 200	
cct gtg ctc atc aag ctg gct tgt gtg ggc acc acg ttt aac gag gct	676
Pro Val Leu Ile Lys Leu Ala Cys Val Gly Thr Thr Phe Asn Glu Ala	
205 210 215	
gag ctt ttt gtg gct agt atc ctt ttc ctt ata gtg cct gtc tca ttc	724
Glu Leu Phe Val Ala Ser Ile Leu Phe Leu Ile Val Pro Val Ser Phe	
220 225 230	
atc ctg gtc tcc tct ggc tac att gcc cac gca gtg ttg agg att aag	772
Ile Leu Val Ser Ser Gly Tyr Ile Ala His Ala Val Leu Arg Ile Lys	
235 240 245	
tca gct acc ggg aga cag aaa gca ttc ggg acc tgc ttc tcc cac ctg	820
Ser Ala Thr Gly Arg Gln Lys Ala Phe Gly Thr Cys Phe Ser His Leu	
250 255 260 265	
aca gtg gtc acc atc ttt tat gga acc atc atc ttc atg tat ctg cag	868
Thr Val Val Thr Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr Leu Gln	
270 275 280	
cca gcc aag agt aga tcc agg gac cag ggc aag ttt gtt tct ctc ttc	916
Pro Ala Lys Ser Arg Ser Arg Asp Gln Gly Lys Phe Val Ser Leu Phe	
285 290 295	
tac act gtg gta acc cgc atg ctt aac cct ctt att tat acc ttg agg	964
Tyr Thr Val Val Thr Arg Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg	
300 305 310	
atc aag gag gtg aaa ggg gca tta aag aaa gtt cta gca aag gct ctg	1012
Ile Lys Glu Val Lys Gly Ala Leu Lys Lys Val Leu Ala Lys Ala Leu	
315 320 325	

gga gta aat att tta tga ttattaaaaa aaaatttaag tgacactgtg atgaa 1065
 Gly Val Asn Ile Leu
 330 335

<210> 8
 <211> 334
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human breast cancer amplified G-protein coupled
 receptor 4 (BCA-GPCR-4)

<400> 8
 Met Cys Tyr Leu Ser Gln Leu Cys Leu Ser Leu Gly Glu His Thr Leu
 1 5 10 15
 His Met Gly Met Val Arg His Thr Asn Glu Ser Asn Leu Ala Gly Phe
 20 25 30
 Ile Leu Leu Gly Phe Ser Asp Tyr Ala Gln Leu Gln Lys Val Leu Phe
 35 40 45
 Val Leu Ile Leu Ile Leu Tyr Leu Leu Thr Ile Leu Gly Asn Thr Thr
 50 55 60
 Ile Ile Leu Val Ser Arg Leu Glu Pro Lys Leu His Met Pro Met Tyr
 65 70 75 80
 Phe Phe Leu Ser His Leu Ser Phe Leu Tyr Arg Cys Phe Thr Ser Ser
 85 90 95
 Val Ile Pro Gln Leu Leu Val Asn Leu Trp Glu Pro Met Lys Thr Ile
 100 105 110
 Ala Tyr Gly Gly Cys Leu Val His Leu Tyr Asn Ser His Ala Leu Gly
 115 120 125
 Ser Thr Glu Cys Val Leu Pro Ala Leu Met Ser Cys Asp Arg Tyr Val
 130 135 140
 Ala Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Ile His Leu
 145 150 155 160
 Cys Met Ala Leu Ala Ser Met Ala Trp Leu Ser Gly Ile Ala Thr Thr
 165 170 175
 Leu Val Gln Ser Thr Leu Thr Leu Gln Leu Pro Phe Cys Gly His Arg
 180 185 190
 Gln Val Asp His Phe Ile Cys Glu Val Pro Val Leu Ile Lys Leu Ala
 195 200 205
 Cys Val Gly Thr Thr Phe Asn Glu Ala Glu Leu Phe Val Ala Ser Ile
 210 215 220
 Leu Phe Leu Ile Val Pro Val Ser Phe Ile Leu Val Ser Ser Gly Tyr
 225 230 235 240
 Ile Ala His Ala Val Leu Arg Ile Lys Ser Ala Thr Gly Arg Gln Lys
 245 250 255
 Ala Phe Gly Thr Cys Phe Ser His Leu Thr Val Val Thr Ile Phe Tyr
 260 265 270
 Gly Thr Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Arg Ser Arg
 275 280 285
 Asp Gln Gly Lys Phe Val Ser Leu Phe Tyr Thr Val Val Thr Arg Met
 290 295 300
 Leu Asn Pro Leu Ile Tyr Thr Leu Arg Ile Lys Glu Val Lys Gly Ala
 305 310 315 320
 Leu Lys Lys Val Leu Ala Lys Ala Leu Gly Val Asn Ile Leu
 325 330

<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-1

<400> 9
atgttgggga acgtcgccat c 21

<210> 10
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-1

<400> 10
tcatccacag agcctccaga t 21

<210> 11
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-2

<400> 11
atgggaaagg acaatccagt t 21

<210> 12
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-2

<400> 12
ctaagagagt aactccagca a 21

<210> 13
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-3

<400> 13
atggaaatag ccaatgtgag ttc 23

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-3

<400> 14
taaatttgcg ccagcttgcc tg 22

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-4

<400> 15
atggtgagac ataccaatga gag 23

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR
amplification primer for BCA-GPCR-4

<400> 16
cataaaatat ttactcccag agcc 24

<210> 17
<211> 1011
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1011)
<223> human breast cancer amplified G-protein coupled
receptor 3-B (BCA-GPCR-3-B)

<400> 17
atg ccc tgt gct ctt ccc aca ggt ggc ctt ttg ccc cac ccc cag cat 48
Met Pro Cys Ala Leu Pro Thr Gly Gly Leu Leu Pro His Pro Gln His
1 5 10 15

aca atg atg gaa ata gcc aat gtg agt tct cca gaa gtc ttt gtc ctc	96
Thr Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu	
20 25 30	
ctg ggc ttc tcc gca cga ccc tca cta gaa act gtc ctc ttc ata gtt	144
Leu Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val	
35 40 45	
gtc ttg agt ttt tac atg gta tgc atc ttg ggc aat ggc atc atc att	192
Val Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile	
50 55 60	
ctg gtc tcc cat aca gat gtg cac ctc cac aca cct atg tac ttc ttt	240
Leu Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe	
65 70 75 80	
ctt gcc aac ctc tcc ttc ctg gac atg agc ttc acc acg agc att gtc	288
Leu Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val	
85 90 95	
cca cag ctc ctg gct aac ctc tgg gga cca cag aaa acc ata agc tat	336
Pro Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr	
100 105 110	
gga ggg tgt gtg gtc cag ttc tat atc tcc cat tgg ctg ggg gca acc	384
Gly Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr	
115 120 125	
gag tgt gtc ctg ctg gcc acc atg tcc tat gac cgc tac gct gcc atc	432
Glu Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile	
130 135 140	
tgc agg cca ctc cat tac act gtc att atg cat cca cag ctt tgc ctt	480
Cys Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu	
145 150 155 160	
ggg cta gct ttg gcc tcc tgg ctg ggg ggt ctg acc acc agc atg gtg	528
Gly Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val	
165 170 175	
ggc tcc acg ctc acc atg ctc cta ccg ctg tgt ggg aac aat tgc atc	576
Gly Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile	
180 185 190	
gac cac ttc ttt tgc gag atg ccc ctc att atg caa ctg gct tgt gtg	624
Asp His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val	
195 200 205	
gat acc agc ctc aat gag atg gag atg tac ctg gcc agc ttt gtc ttt	672
Asp Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe	
210 215 220	
gtt gtc ctg cct ctg ggg ctc atc ctg gtc tct tac ggc cac att gcc	720
Val Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala	
225 230 235 240	
cgg gcc gtg ttg aag atc agg tca gca gaa ggg cgg aga aag gca ttc	768
Arg Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe	
245 250 255	

```

aac acc tgt tct tcc cac gtg gct gtg gtg tct ctg ttt tac ggg agc 816
Asn Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser
      260                      265                      270

atc atc ttc atg tat ctc cag cca gcc aag agc acc tcc cat gag cag 864
Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln
      275                      280                      285

ggc aag ttc ata gct ctg ttc tac acc gta gtc act cct gcg ttg aac 912
Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn
      290                      295                      300

cca ctt att tac acc ctg agg aac acg gag gtg aag agc gcc ctc cgg 960
Pro Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg
      305                      310                      315                      320

cac atg gta tta gag aac tgc tgt ggc tct gca ggc aag ctg gcg caa 1008
His Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln
      325                      330                      335

att
Ile
1011

```

```

<210> 18
<211> 337
<212> PRT
<213> Homo sapiens

```

```

<220>
<223> human breast cancer amplified G-protein coupled
      receptor 3-B (BCA-GPCR-3-B)

```

```

<400> 18
Met Pro Cys Ala Leu Pro Thr Gly Gly Leu Leu Pro His Pro Gln His
 1      5      10
Thr Met Met Glu Ile Ala Asn Val Ser Pro Glu Val Phe Val Leu
      20      25      30
Leu Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val
      35      40      45
Val Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile
      50      55      60
Leu Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe
      65      70      75      80
Leu Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val
      85      90      95
Pro Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr
      100      105      110
Gly Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr
      115      120      125
Glu Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile
      130      135      140
Cys Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu
      145      150      155      160
Gly Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val
      165      170      175
Gly Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile
      180      185      190
Asp His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val
      195      200      205

```

```

Asp Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe
 210                               215                               220
Val Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala
 225                               230                               235                               240
Arg Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe
                               245                               250                               255
Asn Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser
 260                               265                               270
Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln
 275                               280                               285
Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn
 290                               295                               300
Pro Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg
 305                               310                               315                               320
His Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln
                               325                               330                               335
Ile

```

```

<210> 19
<211> 960
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (1)..(960)
<223> human breast cancer amplified G-protein coupled
      receptor 3-C (BCA-GPCR-3-C)

```

```

<400> 19
atg atg gaa ata gcc aat gtg agt tct cca gaa gtc ttt gtc ctc ctg      48
Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
   1                               5                               10                               15

ggc ttc tcc gca cga ccc tca cta gaa act gtc ctc ttc ata gtt gtc      96
Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
                               20                               25                               30

ttg agt ttt tac atg gta tcg atc ttg ggc aat ggc atc atc att ctg     144
Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu
   35                               40                               45

gtc tcc cat aca gat gtg cac ctc cac aca cct atg tac ttc ttt ctt     192
Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
   50                               55                               60

gcc aac ctc tcc ttc ctg gac atg agc ttc acc acg agc att gtc cca     240
Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro
   65                               70                               75                               80

cag ctc ctg gct aac ctc tgg gga cca cag aaa acc ata agc tat gga     288
Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
                               85                               90                               95

ggg tgt gtg gtc cag ttc tat atc tcc cat tgg ctg ggg gca acc gag     336
Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
   100                               105                               110

```


tgt gtc ctg ctg gcc acc atg tcc tat gac cgc tac gct gcc atc tgc	384
Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys	
115 120 125	
agg cca ctc cat tac act gtc att atg cat cca cag ctt tgc ctt ggg	432
Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly	
130 135 140	
cta gct ttg gcc tcc tgg ctg ggg ggt ctg acc acc agc atg gtg ggc	480
Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly	
145 150 155 160	
tcc acg ctc acc atg ctc cta ccg ctg tgt ggg aac aat tgc atc gac	528
Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp	
165 170 175	
cac ttc ttt tgc gag atg ccc ctc att atg caa ctg gct tgt gtg gat	576
His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp	
180 185 190	
acc agc ctc aat gag atg gag atg tac ctg gcc agc ttt gtc ttt gtt	624
Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val	
195 200 205	
gtc ctg cct ctg ggg ctc atc ctg gtc tct tac ggc cac att gcc cgg	672
Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg	
210 215 220	
gcc gtg ttg aag atc agg tca gca gaa ggg cgg aga aag gca ttc aac	720
Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn	
225 230 235 240	
acc tgt tct tcc cac gtg gct gtg gtg tct ctg ttt tac ggg agc atc	768
Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile	
245 250 255	
atc ttc atg tat ctc cag cca gcc aag agc acc tcc cat gag cag ggc	816
Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly	
260 265 270	
aag ttc ata gct ctg ttc tac acc gta gtc act cct gcg ttg aac cca	864
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro	
275 280 285	
ctt att tac acc ctg agg aac acg gag gtg aag agc gcc ctc cgg cac	912
Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His	
290 295 300	
atg gta tta gag aac tgc tgt ggc tct gca ggc aag ctg gcg caa att	960
Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile	
305 310 315 320	

<210> 20

<211> 320

<212> PRT

<213> Homo sapiens

<220>

<223> human breast cancer amplified G-protein coupled
receptor 3-C (BCA-GPCR-3-C)

<400> 20

```

Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
 1           5           10           15
Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
           20           25           30
Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu
           35           40           45
Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
           50           55           60
Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro
           65           70           75           80
Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
           85           90           95
Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
           100           105           110
Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys
           115           120           125
Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly
           130           135           140
Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly
           145           150           155           160
Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp
           165           170           175
His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp
           180           185           190
Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val
           195           200           205
Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg
           210           215           220
Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn
           225           230           235           240
Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile
           245           250           255
Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly
           260           265           270
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro
           275           280           285
Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His
           290           295           300
Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile
           305           310           315           320

```

<210> 21

<211> 957

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(957)

<223> human breast cancer amplified G-protein coupled
receptor 3-D (BCA-GPCR-3-D)

<400> 21

```

atg gaa ata gcc aat gtg agt tct cca gaa gtc ttt gtc ctc ctg ggc
Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu Gly
 1           5           10           15

```

48

ttc tcc gca cga ccc tca cta gaa act gtc ctc ttc ata gtt gtc ttg	96
Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val Leu	
20 25 30	
agt ttt tac atg gta tcg atc ttg ggc aat ggc atc atc att ctg gtc	144
Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu Val	
35 40 45	
tcc cat aca gat gtg cac ctc cac aca cct atg tac ttc ttt ctt gcc	192
Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ala	
50 55 60	
aac ctc tcc ttc ctg gac atg agc ttc acc acg agc att gtc cca cag	240
Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro Gln	
65 70 75 80	
ctc ctg gct aac ctc tgg gga cca cag aaa acc ata agc tat gga ggg	288
Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly	
85 90 95	
tgt gtg gtc cag ttc tat atc tcc cat tgg ctg ggg gca acc gag tgt	336
Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys	
100 105 110	
gtc ctg ctg gcc acc atg tcc tat gac cgc tac gct gcc atc tgc agg	384
Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg	
115 120 125	
cca ctc cat tac act gtc att atg cat cca cag ctt tgc ctt ggg cta	432
Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly Leu	
130 135 140	
gct ttg gcc tcc tgg ctg ggg ggt ctg acc acc agc atg gtg ggc tcc	480
Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly Ser	
145 150 155 160	
acg ctc acc atg ctc cta ccg ctg tgt ggg aac aat tgc atc gac cac	528
Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His	
165 170 175	
ttc ttt tgc gag atg ccc ctc att atg caa ctg gct tgt gtg gat acc	576
Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr	
180 185 190	
agc ctc aat gag atg gag atg tac ctg gcc agc ttt gtc ttt gtt gtc	624
Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val	
195 200 205	
ctg cct ctg ggg ctc atc ctg gtc tct tac ggc cac att gcc cgg gcc	672
Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala	
210 215 220	
gtg ttg aag atc agg tca gca gaa ggg cgg aga aag gca ttc aac acc	720
Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr	
225 230 235 240	
tgt tct tcc cac gtg gct gtg gtg tct ctg ttt tac ggg agc atc atc	768
Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile	
245 250 255	

ttc atg tat ctc cag cca gcc aag agc acc tcc cat gag cag ggc aag 816
 Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys
 260 265 270

ttc ata gct ctg ttc tac acc gta gtc act cct gcg ttg aac cca ctt 864
 Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285

att tac acc ctg agg aac acg gag gtg aag agc gcc ctc cgg cac atg 912
 Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His Met
 290 295 300

gta tta gag aac tgc tgt ggc tct gca ggc aag ctg gcg caa att 957
 Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile
 305 310 315

<210> 22

<211> 319

<212> PRT

<213> Homo sapiens

<220>

<223> human breast cancer amplified G-protein coupled
receptor 3-D (BCA-GPCR-3-D)

<400> 22

Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu Gly
 1 5 10 15
 Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val Leu
 20 25 30
 Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu Val
 35 40 45
 Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
 50 55 60
 Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro Gln
 65 70 75 80
 Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly
 85 90 95
 Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys
 100 105 110
 Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg
 115 120 125
 Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly Leu
 130 135 140
 Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly Ser
 145 150 155 160
 Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His
 165 170 175
 Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr
 180 185 190
 Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val
 195 200 205
 Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala
 210 215 220
 Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr
 225 230 235 240
 Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile
 245 250 255
 Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys
 260 265 270

Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
275 280 285
Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His Met
290 295 300
Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile
305 310 315

<210> 23
<211> 1020
<212> DNA
<213> Homo sapiens

<220>
<223> human breast cancer amplified G-protein coupled
receptor 3-A (BCA-GPCR-3-A) cDNA

<220>
<221> CDS
<222> (1)..(1020)
<223> human breast cancer amplified G-protein coupled
receptor 3-A (BCA-GPCR-3-A)

<400> 23
atgccctgta tgccctgtgc tcttcccaca ggtggccttt tgccccaccc ccagcataca 60
atgatggaaa tagccaatgt gagttctcca gaagtctttg tcctcctggg cttctccgca 120
cgaccctcac tagaaactgt cctcttcata gttgtcttga gtttttacat ggtatcgatc 180
ttggggcaatg gcatcatcat tctgggtctcc catcacagatg tgcacctcca cacacctatg 240
tacttctttc ttgccaacct ctcttctctg gacatgagct tcaccacgag cattgtccca 300
cagctcctgg ctaacctctg gggaccacag aaaaccataa gctatggagg gtgtgtgggtc 360
cagttctata tctcccattg gctgggggga accgagtgtg tcctgctggc caccatgtcc 420
tatgaccgct acgctgccat ctgcaggcca ctccattaca ctgtcattat gcatccacag 480
ctttgccttg ggctagcttt ggctcctctg ctgggggggtc tgaccaccag catggtgggc 540
tccacgctca ccatgctcct accgctgtgt gggaacaatt gcatcgacca cttcttttgc 600
gagatgcccc tcattatgca actggcttgt gtggatacca gcctcaatga gatggagatg 660
tacctggcca gctttgtctt tgttgtctct cctctggggc tcctcctggt ctcttacggc 720
cacattgccc gggccgtggt gaagatcagg tcagcagaag ggcggagaaa ggcattcaac 780
acctgttctt cccacgtggc tgtggtgtct ctgttttacg ggagcatcat cttcatgtat 840
ctccagccag ccaagagcac ctcccatgag cagggaaggt tcatagctct gttctacacc 900
gtagtcactc ctgcgttgaa cccacttatt tacacctga ggaacacgga ggtgaagagc 960
gcctccggc acatgggtatt agagaactgc tgtggctctg caggcaagct ggcgcaaatt 1020